Serial No. 09/766,399
Group Art Unit: 1634

Version with markings to show changes made

WHAT IS CLAIMED IS:

1. [Cancelled]

2. (Amended) An isolated [The] plant promoter [of Claim 1] comprising at least one synthetic multimeric promoter element region [having a nucleotide sequence] that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

[(a) a nucleotide sequence comprising promoter elements DRE1, ABRE1, DRE1, As-1, ABRE1, DRE1, GT-2, As-1, DRE1, PCNA IIA, PCNA IIA, DRE1, As-1, and DRE1 sequentially (SEQ ID NO.: 66);

(b) a nucleotide sequence comprising promoter elements DRE1, DRE1, As-1, PCNA IIA, ABRE1, PCNA IIA, ABRE1, DRE1, GT-2, GT-2, and ABRE1 sequentially (SEQ ID NO.: 67);]

[(c)] (a)a nucleotide sequence comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.: 2, ABRE1 comprising SEQ ID NO.: 2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.: 7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, As-1 comprising SEQ ID NO.: 7, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, and ABRE1 comprising SEQ ID NO.: 2, sequentially; comprising [(SEQ ID NO.: 65)];

(b) a nucleotide sequence comprising SEQ ID NO.: 65;

[(d) a nucleotide sequence comprising promoter elements ABRE1, ABRE1, GT-2, GT-2, GT-2, DRE1, DRE1, DRE1, DRE1, ABRE1 , and PCNA IIA sequentially (SEQ ID NO.: 68);

(e) a nucleotide sequence comprising promoter elements PCNA IIA, As-1, GT-2, As-1, DRE1, As-1, As-1, PCNA IIA, As-1, PCNA IIA, DRE1, and ABRE1 sequentially (SEQ ID NO.: 69);

(f) a nucleotide sequence comprising promoter elements As-1, GT-2, DRE1, DRE1, ABRE1, PCNA IIA, DRE1, PCNA IIA, ABRE1, DRE1, and DRE1 sequentially (SEQ ID NO.: 71);

(g) a nucleotide sequence comprising promoter elements As-1, ABRE1, GT-2, As-1, ABRE1, and DRE1 sequentially (SEQ ID NO.: 72);

(h) a nucleotide sequence comprising promoter elements DRE1, ABRE1, GT-2, DRE1, As-1, As-1, and As-1 sequentially (SEQ ID NO.: 70);

(i) a nucleotide sequence set forth in Figure 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72);

(j) a nucleotide sequence that comprises a variant of a nucleotide sequence set forth in Figure 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72); and]

[(k)](c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to a nucleotide sequence of (a)[,]or (b)[, (c), (d), (e), (f), (g), (h), (i), or (j)], wherein said stringent conditions include hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60-65°C; and

(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or (b).

7. (Amended) A plant, or its parts, having stably incorporated into its genome a DNA construct comprising a plant promoter of claim 2 operably linked to a coding sequence[, said plant promoter comprising at least one synthetic multimeric promoter element region (SMPER) that enhances expression of said coding sequence].

8. (Amended) A plant, or its parts, having stably incorporated into its genome a DNA construct comprising a plant promoter operably linked to a coding sequences, said plant promoter comprising at least one synthetic multimeric promoter element region [having a nucleotide sequence] that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

[(a) a nucleotide sequence comprising promoter elements DRE1, ABRE1, DRE1, As-1, ABRE1, DRE1, GT-2, As-1, DRE1, PCNA IIA, PCNA IIA, DRE1, As-1, and DRE1 sequentially (SEQ ID NO.: 66);

(b) a nucleotide sequence comprising promoter elements DRE1, DRE1, As-1, PCNA IIA, ABRE1, PCNA IIA, ABRE1, DRE1, GT-2, GT-2, and ABRE1 sequentially (SEQ ID NO.: 67);]

[(c)] (a)a nucleotide sequence comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.: 2, ABRE1 comprising SEQ ID NO.: 2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.: 7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, As-1 comprising SEQ ID NO.: 7, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, and ABRE1 comprising SEQ ID NO.: 2, sequentially [(SEQ ID NO.: 65)];

(b) a nucleotide sequence comprising SEQ ID NO.: 65;

[(d) a nucleotide sequence comprising promoter elements ABRE1, ABRE1, GT-2, GT-2, GT-2, DRE1, DRE1, DRE1, DRE1, ABRE1, and PCNA IIA sequentially (SEQ ID NO.: 68);

(e) a nucleotide sequence comprising promoter elements PCNA IIA, As-1, GT-2, As-1, DRE1, As-1, As-1, PCNA IIA, As-1, PCNA IIA, DRE1, and ABRE1 sequentially (SEQ ID NO.: 69);

(f) a nucleotide sequence comprising promoter elements As-1, GT-2, DRE1, DRE1, ABRE1, PCNA IIA, DRE1, PCNA IIA, ABRE1, DRE1, and DRE1 sequentially (SEQ ID NO.: 71);

(g) a nucleotide sequence comprising promoter elements As-1, ABRE1, GT-2, As-1, ABRE1, and DRE1 sequentially (SEQ ID NO.: 72);

(h) a nucleotide sequence comprising promoter elements DRE1, ABRE1, GT-2, DRE1, As-1, As-1, and As-1 sequentially (SEQ ID NO.: 70);

(i) a nucleotide sequence set forth in Figure 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72);

(j) a nucleotide sequence that comprises a variant of a nucleotide sequence set forth in Figures 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72); and]

[(k)](c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to a nucleotide sequence of (a)[,]or (b)[,(c), (d), (e), (f), (g), (h), (i), or (j)], wherein said stringent conditions include hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60-65°C; and

(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or (b).

12. (Amended) A plant cell having stably incorporated into its genome a DNA construct comprising a plant promoter operably linked to a coding sequence, said plant promoter comprising at least one synthetic multimeric promoter element region [having a nucleotide sequence] that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

[(a) a nucleotide sequence comprising promoter elements DRE1, ABRE1, DRE1, As-1, ABRE1, DRE1, GT-2, As-1, DRE1, PCNA IIA, PCNA IIA, DRE1, As-1, and DRE1 sequentially (SEQ ID NO.: 66);

(b) a nucleotide sequence comprising promoter elements DRE1, DRE1, As-1, PCNA IIA, ABRE1, PCNA IIA, ABRE1, DRE1, GT-2, GT-2, and ABRE1 sequentially (SEQ ID NO.: 67);]

[(c)](a) a nucleotide sequence comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.: 2, ABRE1 comprising SEQ ID NO.: 2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.: 7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, As-1 comprising SEQ ID NO.: 7, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, and ABRE1 comprising SEQ ID NO.: 2, sequentially [(SEQ ID NO.: 65)];

(b) a nucleotide sequence comprising SEQ ID NO.: 65;

[(d) a nucleotide sequence comprising promoter elements ABRE1, ABRE1, GT-2, GT-2, GT-2, DRE1, DRE1, DRE1, DRE1, ABRE1 and PCNA IIA sequentially (SEQ ID NO.: 68);

(e) a nucleotide sequence comprising promoter elements PCNA IIA, As-1, GT-2, As-1, DRE1, As-1, As-1, PCNA IIA, As-1, PCNA IIA, DRE1, and ABRE1 sequentially (SEQ ID NO.: 69);

(f) a nucleotide sequence comprising promoter elements As-1, GT-2, DRE1, DRE1, ABRE1, PCNA IIA, DRE1, PCNA IIA, ABRE1, DRE1, and DRE1 sequentially (SEQ ID NO.: 71);

(g) a nucleotide sequence comprising promoter elements As-1, ABRE1, GT-2, As-1, ABRE1, and DRE1 sequentially (SEQ ID NO.: 72);

(h) a nucleotide sequence comprising promoter elements DRE1, ABRE1, GT-2, DRE1, As-1, As-1, and As-1 sequentially (SEQ ID NO.: 70);

(i) a nucleotide sequence set forth in Figure 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72);

(j) a nucleotide sequence that comprises a variant of a nucleotide sequence set forth in Figure 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72); and]

[(k)](c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to the nucleotide sequence of (a)[,] or (b)[, (c), (d), (e), (f), (g), (h), (i), or (j)]), wherein said stringent conditions include hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60-65°C; and

(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or (b).

16. (Amended) A method for constitutively expressing a heterologous nucleotide sequence in a plant, said method comprising:

[(i)] (a) transforming a plant cell with a transformation vector comprising an expression cassette, said expression cassette comprising a plant promoter of claim 2 operably linked to a coding sequence[, said plant promoter comprising a synthetic multimeric promoter element region [selected from the group consisting of (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), and (k) of claim 1]; and

[(ii)] (b)regenerating a stably transformed plant from said transformed cell, said plant having stably incorporated into its genome said expression cassette.

17. [Cancelled]

18. [Cancelled]